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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=9; day=11; hr=14; min=23; sec=23; ms=624;]

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Reviewer Comments:

<210> 23

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> PP2A motif

<220>

<221> misc_feature

<222> (3)..(3)

<223> Xaa can be any naturally occurring amino acid

<400> 23

Gly Asp Xaa His Gly Gln

1

5

Although the above "<211>" response is "7", only 6 amino acids are shown above.

Application No: 10590551 Version No: 3.0

Input Set:

Output Set:

Started: 2009-08-27 18:04:53.801
Finished: 2009-08-27 18:04:55.734
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 933 ms
Total Warnings: 15
Total Errors: 1
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
E 331	Count of Protein differs from the <211> tag Input: 7 Calculated:
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

SEQUENCE LISTING

<110> Genomine, Inc.
POSTECH FOUNDATION

<120> Novel Phytochrome-interacting protein and a use thereof

<130> OP05-1002

<140> 10590551

<141> 2009-08-27

<150> KR10-2004-0013663

<151> 2004-02-27

<160> 26

<170> KopatentIn 1.71

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

ggatccaaat gtcaggctct aggccgact

29

<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 2

ctcgagctac ttgtttgctg cagcgagttc

30

<210> 3

<211> 1455

<212> DNA

<213> Arabidopsis thaliana

<400> 3

atggagacca agaatgagaa ttctgatgtt tcacgggcag aggagtttaa aagtcaggcc

60

aacgaagctt ttaaagggtca caaatactcc agtgctattg atctatatac aaaagctatt

120

gaactcaaca gcaacaacgc tgtgtattgg gcaaactcgtg catttgctca cacaaaactg

180

gaggaatatg gcagtgcaat acaggatgca tcgaaggcca ttgaagttga ttcaagatac	240
tctaagggct attacaggcg tgggtgctgcg tatcttgcca tgggaaaatt taaggatgcc	300
ttgaaggact tccaacaggt aaaaaggctt tctcctaattg accctgatgc cacaagaaag	360
ctaaaggaat gtgagaaagc agtgatgaaa ctcaaatttg aagaagcaat ctctgtgcca	420
gtatctgaaa ggcgttcagt agctgagtc attgacttcc atacaataga ggttgagcca	480
caatattctg gtgctagaat tgagggagag gaagttacct tagattttgt gaaaacgatg	540
atggaggatt ttaagaacca aaaaacattg cataaacggg atgcctatca aatcgtctta	600
cagactaggc aaatcttgct agcaactgct tctcttggtg atataagtgt tccacatggc	660
aaacatatca ctgtttgcgg tgacgttcat ggtcagttct acgatcttct caatatcttt	720
gagcttaatg gcctcccttc ggaggagaac ccatacctat ttaatggcga ctttgtggac	780
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tcatccatat atctagccag aggaaacct gaaagcaaga gcatgaacaa aatttatggt	900
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cttttcagtg ttgacggcgt gaaactctca gacatcagag ccattgacag attctgtgag	1080
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ttgcaagata acaatttaga tttgttggtc cggtcacatg aagtaaaaga tgaaggttat	1260
gaggttgaac atgacggtaa actcataact gtcttctctg cgccaaatta ctgtgatcag	1320
atgggtaata agggagcctt cattcgtttt gaagctctg atatgaagcc aaacattggt	1380
acattctcag cagtgcctca tccggatgtg aagcctatgg catatgcaa caactttctc	1440
aggatgttca actaa	1455

<210> 4
 <211> 484
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4
 Met Glu Thr Lys Asn Glu Asn Ser Asp Val Ser Arg Ala Glu Glu Phe
 1 5 10 15
 Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
 20 25 30

Ile	Asp	Leu	Tyr	Thr	Lys	Ala	Ile	Glu	Leu	Asn	Ser	Asn	Asn	Ala	Val	35	40	45
Tyr	Trp	Ala	Asn	Arg	Ala	Phe	Ala	His	Thr	Lys	Leu	Glu	Glu	Tyr	Gly	50	55	60
Ser	Ala	Ile	Gln	Asp	Ala	Ser	Lys	Ala	Ile	Glu	Val	Asp	Ser	Arg	Tyr	65	70	75
Ser	Lys	Gly	Tyr	Tyr	Arg	Arg	Gly	Ala	Ala	Tyr	Leu	Ala	Met	Gly	Lys	85	90	95
Phe	Lys	Asp	Ala	Leu	Lys	Asp	Phe	Gln	Gln	Val	Lys	Arg	Leu	Ser	Pro	100	105	110
Asn	Asp	Pro	Asp	Ala	Thr	Arg	Lys	Leu	Lys	Glu	Cys	Glu	Lys	Ala	Val	115	120	125
Met	Lys	Leu	Lys	Phe	Glu	Glu	Ala	Ile	Ser	Val	Pro	Val	Ser	Glu	Arg	130	135	140
Arg	Ser	Val	Ala	Glu	Ser	Ile	Asp	Phe	His	Thr	Ile	Glu	Val	Glu	Pro	145	150	155
Gln	Tyr	Ser	Gly	Ala	Arg	Ile	Glu	Gly	Glu	Glu	Val	Thr	Leu	Asp	Phe	165	170	175
Val	Lys	Thr	Met	Met	Glu	Asp	Phe	Lys	Asn	Gln	Lys	Thr	Leu	His	Lys	180	185	190
Arg	Tyr	Ala	Tyr	Gln	Ile	Val	Leu	Gln	Thr	Arg	Gln	Ile	Leu	Leu	Ala	195	200	205
Leu	Pro	Ser	Leu	Val	Asp	Ile	Ser	Val	Pro	His	Gly	Lys	His	Ile	Thr	210	215	220
Val	Cys	Gly	Asp	Val	His	Gly	Gln	Phe	Tyr	Asp	Leu	Leu	Asn	Ile	Phe	225	230	235
Glu	Leu	Asn	Gly	Leu	Pro	Ser	Glu	Glu	Asn	Pro	Tyr	Leu	Phe	Asn	Gly	245	250	255
Asp	Phe	Val	Asp	Arg	Gly	Ser	Phe	Ser	Val	Glu	Ile	Ile	Leu	Thr	Leu	260	265	270
Phe	Ala	Phe	Lys	Cys	Met	Cys	Pro	Ser	Ser	Ile	Tyr	Leu	Ala	Arg	Gly	275	280	285
Asn	His	Glu	Ser	Lys	Ser	Met	Asn	Lys	Ile	Tyr	Gly	Phe	Glu	Gly	Glu	290	295	300
Val	Arg	Ser	Lys	Leu	Ser	Glu	Lys	Phe	Val	Asp	Leu	Phe	Ala	Glu	Val	305	310	315
Phe	Cys	Tyr	Leu	Pro	Leu	Ala	His	Val	Ile	Asn	Gly	Lys	Val	Phe	Val	325	330	335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
 340 345 350
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
 355 360 365
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430
 Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
 435 440 445
 Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
 450 455 460
 Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu
 465 470 475 480
 Arg Met Phe Asn

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 5
 ggatccatgg agaccaagaa tgag

24

<210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 6
 ctcgagttag ttgaacatcc tgag

24

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
ggatccgatg tcaggctcta ggccgact

28

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8
gctgatcagc atggtttccg gagtcggggg tagt

34

<210> 9
<211> 34
<212> DNA
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<220>
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<400> 9
cccggccgga ctaatatggc atcatcagca tcat

34

<210> 10
<211> 27
<212> DNA
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<220>
<223> PCR primer

<400> 10
ctcgagtcaa gagattgctt cttcaaa

27

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 11
 ggatccatgc cagtatctga aaggcgt 27

<210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 12
 atggagacca agaatgagaa ttct 24

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 13
 ttagttgaac atcctgagaa agtt 24

<210> 14
 <211> 347
 <212> PRT
 <213> Arabidopsis thaliana

<400> 14
 Ser Val Pro Val Ser Glu Arg Arg Ser Val Ala Glu Ser Ile Asp Phe
 1 5 10 15
 His Thr Ile Glu Val Glu Pro Gln Tyr Ser Gly Ala Arg Ile Glu Gly
 20 25 30
 Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys
 35 40 45
 Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln
 50 55 60
 Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val
 65 70 75 80
 Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe

85										90					95				
Tyr	Asp	Leu	Leu	Asn	Ile	Phe	Glu	Leu	Asn	Gly	Leu	Pro	Ser	Glu	Glu				
			100						105					110					
Asn	Pro	Tyr	Leu	Phe	Asn	Gly	Asp	Phe	Val	Asp	Arg	Gly	Ser	Phe	Ser				
		115				120						125							
Val	Glu	Ile	Ile	Leu	Thr	Leu	Phe	Ala	Phe	Lys	Cys	Met	Cys	Pro	Ser				
	130					135						140							
Ser	Ile	Tyr	Leu	Ala	Arg	Gly	Asn	His	Glu	Ser	Lys	Ser	Met	Asn	Lys				
145					150					155					160				
Ile	Tyr	Gly	Phe	Glu	Gly	Glu	Val	Arg	Ser	Lys	Leu	Ser	Glu	Lys	Phe				
			165					170						175					
Val	Asp	Leu	Phe	Ala	Glu	Val	Phe	Cys	Tyr	Leu	Pro	Leu	Ala	His	Val				
		180						185					190						
Ile	Asn	Gly	Lys	Val	Phe	Val	Val	His	Gly	Gly	Leu	Phe	Ser	Val	Asp				
	195						200					205							
Gly	Val	Lys	Leu	Ser	Asp	Ile	Arg	Ala	Ile	Asp	Arg	Phe	Cys	Glu	Pro				
	210					215				220									
Pro	Glu	Glu	Gly	Leu	Met	Cys	Glu	Leu	Leu	Trp	Ser	Asp	Pro	Gln	Pro				
225					230					235					240				
Leu	Pro	Gly	Arg	Gly	Pro	Ser	Lys	Arg	Gly	Val	Gly	Leu	Ser	Phe	Gly				
			245						250					255					
Gly	Asp	Val	Thr	Lys	Arg	Phe	Leu	Gln	Asp	Asn	Asn	Leu	Asp	Leu	Leu				
		260						265					270						
Val	Arg	Ser	His	Glu	Val	Lys	Asp	Glu	Gly	Tyr	Glu	Val	Glu	His	Asp				
		275					280						285						
Gly	Lys	Leu	Ile	Thr	Val	Phe	Ser	Ala	Pro	Asn	Tyr	Cys	Asp	Gln	Met				
	290					295					300								
Gly	Asn	Lys	Gly	Ala	Phe	Ile	Arg	Phe	Glu	Ala	Pro	Asp	Met	Lys	Pro				
305					310					315					320				
Asn	Ile	Val	Thr	Phe	Ser	Ala	Val	Pro	His	Pro	Asp	Val	Lys	Pro	Met				
			325					330					335						
Ala	Tyr	Ala	Asn	Asn	Phe	Leu	Arg	Met	Phe	Asn									
		340						345											

<210> 15
 <211> 1041
 <212> DNA
 <213> Arabidopsis thaliana

 <400> 15

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acgatgatgg aggatttttaa gaacccaaaa acattgcata aacggtatgc ctatcaaatac	180
gtcttacaga ctaggcaaata cttgctagca ctgccttctc ttgttgatat aagtgttcca	240
catggcaaac atatcactgt ttgcggtgac gttcatgggc agttctacga tcttctcaat	300
atctttgagc ttaatggcct cccttcggag gagaacccat acctatttaa tggcgacttt	360
gtggacagag gctcattctc cgttgagatc atcctcactt tgtttgcttt caagtgcattg	420
tgcccatcat ccataatatc agccagagga aaccatgaaa gcaagagcat gaacaaaatt	480
tatgggttttg agggtgaggt tcgggtccaag ttgagtgaaa aattcgtgga tctctttgct	540
gaagttttct gttacctccc gttggctcat gttataaatg ggaaggctct cgtgggtacat	600
ggaggtcttt tcagtgttga cggcgtgaaa ctctcagaca tcagagccat tgacagattc	660
tgtgagccac cagaggaagg actaatgtgt gaactattgt ggagtgatec tcaacctctc	720
cctggaagag gcccaagcaa gcgaggaggt ggtctatcat ttggtggaga tgtgacaaaag	780
aggtttttgc aagataacaa tttagatttg ttgggtccggc cacatgaagt aaaagatgaa	840
ggttatgagg ttgaacatga cggtaaaactc ataactgtct tctctgcgcc aaattactgt	900
gatcagatgg gtaataaggg agccttcatt cgttttgaag ctctgatata gaagccaaac	960
attgttacat tctcagcagt gcctcatccg gatgtgaagc ctatggcata tgcaaacaac	1020
tttctcagga tgttcaacta a	1041

<210> 16
 <211> 479
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)
 <223> PAPP5

<400> 16
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 Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
 20 25 30
 Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
 35 40 45

Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
50 55 60

Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
65 70 75 80

Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
85 90 95

Glu Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Gly Leu Ser Pro
100 105 110

Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
115 120 125

Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
130 135 140

Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
145 150 155 160

Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
165 170 175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
180 185 190

Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
195 200 205

Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
210 215 220

Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
225 230 235 240

Glu Asp Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
245 250 255

Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
260 265 270

Phe Ala Glu Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
275 280 285

Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
290 295 300

Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
305 310 315 320

Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
325 330 335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
340 345 350

Arg Ala Ile Asp Arg Phe Cys Glu Pro Phe Glu Glu Gly Leu Met Cys
 355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430

Ser Ala Pro Asn Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile Arg
 435 440 445

Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala Val
 450 455 460

Pro His Pro Met Ala Tyr Ala Asn Asn Phe Ile Arg Met Phe Asn
 465 470 475

<210> 17
 <211> 492
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)
 <223> PP5

<400> 17

Glu Arg Thr Glu Cys Ala Glu Pro Pro Arg Asp Glu Pro Pro Ala Asp
 1 5 10 15

Gly Ala Leu Lys Arg Ala Glu Glu Leu Lys Thr Gln Ala Asn Asp Tyr
 20 25 30

Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile Lys Phe Tyr Ser Gln Ala
 35 40 45

Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr Tyr Gly Asn Arg Ser Leu
 50 55 60

Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr Ala Leu Gly Asp Ala Thr
 65 70 75 80

Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile Lys Gly Tyr Tyr Arg Arg
 85 90 95

Ala Ala Ser Asn Met Ala Leu Gly Lys Phe Arg Ala Ala Leu Arg Asp

100

105

110

Tyr Glu Thr Val Val Lys Val Lys Pro